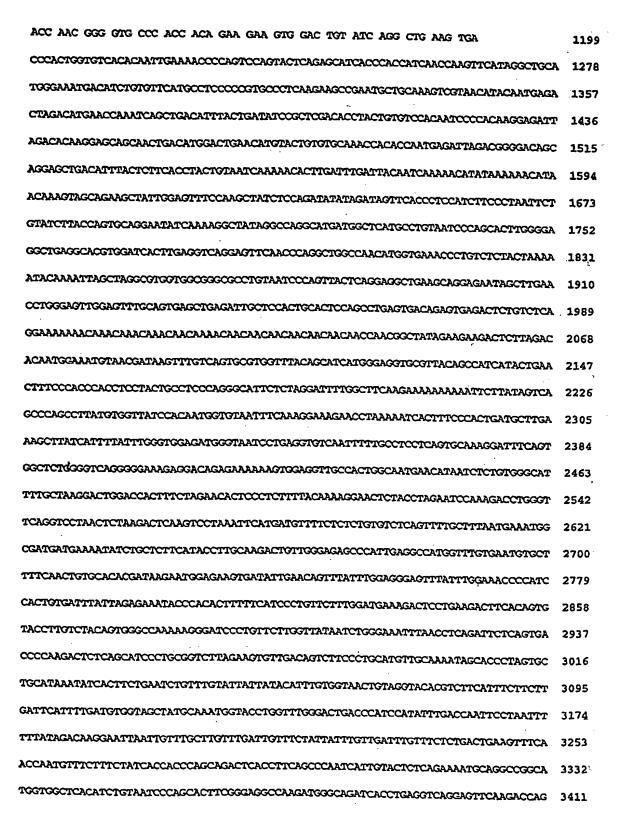
M A A Q N G N T Q D H A S S L S P N F SFTPNFNPP AGT TTC ACA CCC AAC TIT AAT CCA CCC CAA GAC CAT GCC TCC, TCC CTC TCC TIT AAC TTC 128 PMDEDEDMTKTRT 48 GDYDL AGT TAT GOT GAT TAT GAC CTC CCT ATG GAT GAG GAT GAG GAC ATG ACC AAG ACC CGG ACC 188 A K I V I G I A L A G I M L V C G 68 TTC TTC GCA GCC AAG ATC GTC ATT GGC ATT GCA CTG GCA GGC ATC ATG CTG GTC TGC GGC 248 G N F V F I A A L T R Y K K L R N L T 88 ATC GOT AAC TIT GIC TIT ATC GCT GCC CTC ACC CGC TAT AAG AAG TIG CGC AAC CTC ACC 30B SDFLVAI 108 NLLIANL A AAT CTG CTC ATT GCC AAC CTG GCC ATC TCC GAC TTC CTG GTG GCC ATC ATC TGC TGC CCC 368 FEMDYYVVRQLSWEHGHVLC 128 TTC CAG ATG CAC TAC TAC GTG GTA COG CAG CTC TCC TGG GAG CAT GGC CAC GTG CTC TGT 428 A S V N Y L R T V S L Y V S T N A L 148 GCC TCC GTC AAC TAC CTG CGC ACC GTC TCC CTC TAC GTC TCC ACC AAT GCC TTG CTG GCC 488 AIDRYLAIVHPLKPRMNYQ 168 ATT GCC ATT GAC AGA TAT CTC GCC ATC GTT CAC CCC TTG AAA CCA CGG ATG AAT TAT CAA 548 TASFLIALVWMVSILIAIPS 188 ACG GCC TCC TTC CTG ATC GCC TTG GTC TGG ATG GTG TCC ATT CTC ATT GCC ATC CCA TCG 608 A.Y FATETVLFIVKSQEKIFC 208 GCT TAC TIT GCA ACA GAA ACC GTC CTC TIT ATT GTC AAG AGC CAG GAG AAG ATC TTC TGT 668 I W P V D Q Q L Y Y K S Y F. 228 GGC CAG ATC TGG CCT GTG GAT CAG CAG CTC TAC TAC AAG TCC TAC TTC CTC TTC ATC TTT **728** VTMTLCYARI 248 GVEFVG GGT GTC GAG TTC GTG GGC CCT GTG GTC ACC ATG ACC CTG TGC TAT GCC AGG ATC TCC CGG 788 P G F Q T E Q I R K R L R 268 K A V GAG CTC TGG TTC AAG GCA GTC CCT GGG TTC CAG ACG GAG CAG ATT CGC AAG CGG CTG CGC 848 C R R K T V L V L M C I L T A Y V L C W 288 TOC COC AGG AAG ACG GTC CTG GTG CTC ATG TGC ATT CTC ACG GCC TAT GTG CTG TGC TGG 908 APFYGFTIVRDFFPTVFVKE 308 SCA CCC TTC TAC GOT TTC ACC ATC GTT CGT GAC TTC TTC CCC ACT GTG TTC GTG AAG GAA 968 328 YVVECIAMSNSMI K H Y L T A F ANG CAC TAC CTC ACT GCC TTC TAC GTG GTC GAG TGC ATC GCC ATG AGC AAC AGC ATG ATC 1028 N T V C F V T V K N N T M K Y F K K M M AAC ACC GTG TGC TTC GTG ACG GTC AAG AAC AAC ACC ATG AAG TAC TTC AAG AAG ATG ATG 368 LLHWRPSQRGSKS SADLDLR CTG CTG CAC TGG CGT CCC TCC CAG CGG GGG AGC AAG TCC AGT GCT GAC CTT GAC CTC AGA 1148 385 E E V D C R T



IGGCCAACATGGCAAAACOCCATCTCTAGAAAAATACAGAAATTAGCTGGCGTGGTGGCACATGCCTGTGGTCCCAG	3490
CTCAGGAGGCTGAGGCATGAGAATTGCTTGAACCCCAGAGGCAGAGGTTGCAGTGAATTGAGATGGCACCACTGCA	3569
CAGCTTGGGTGATAGAGCAAGATTCCATCTCAAAAGGAAAATAAAAGAAAATGCAAACACACTATAATATTAGCCT	3648
SCANALTGTTAATTCTGATTTACAAAAATTCTTACTTGGCTTTGAAATGCATTGTGTAATAATGCATTTCAA	3727
CAAGCAAGTAACAATTTTAGGTTATGTACATTTCTATAAATAA	3806
CTTAGCCGAATCAGGAGATTCTTTAGGAATGGACCATGTACCAGTCAAGTCTGTCAGCAGGATTCATCACCCTGTT	3885
TTTTGTCCTAGAATATACCAACTTCCTTTCATTGAAATTTAACTGAAAAAACTTTTGTAAATATCAGTGTGTATTT	3964
DAKAKAKAKAKATTAKEOTETGATAKATAKATTAKTTAKATAKATAKATAKATAKATAKA	4043
poscosc .	4052

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GAATTCCCGGGTCGACCCACGCGTCCGGGCGGCGGAACTCCCGCTTATTGGTCCCCGGTGGCGATCTTTGGGAGACCA ATAGACGCCCCAGAGGGAGGACACTGGGATCCAGACTCCACTGGAACCCCGCTTTTCAGATCCTGGATGGTATCTGTTC 158 TCCCTAAGGATTCTAACAGGGACCTGCACTCACTGACCCCAGCAGAAGTGCTGAACTCCACGTGAGCGCATCTCCCTGA 237 12 TACACACCAGCCCACCTGTAGCATCATCAAC ATG GGA CCC CAG AAC AGA AAC ACT AGC TTT GCA CCA 304 D 32 GAC TTG AAT CCA CCC CAA GAC CAT GTC TCC TTA AAC TAC AGT TAT GGT GAT TAT GAC CTC 364 D E D т K Α ĸ I 52 CCC CTG GGT GAG GAT GAG GAT GTG ACC AAG ACA CAG ACC TTC TTT GCA GCC AAA ATT GTC 424 1 G I M L v C I 72 ATT GGC GTG GCA CTG GCA GGC ATC ATG CTG GTC TGC GGC ATT GGC AAC TTT GTC TTC ATT 484 Y K K L R; N 92 GCT GCC CTC GCC CGC TAC AAG AAG CTG CGC AAC CTT ACC AAC CTC CTC ATT GCT AAC CTG 544 112 GCC ATC TCT GAC TTC CTG GTG GCG ATC GTC TGC TGC CCC TTT GAG ATG GAC TAT TAT GTA 604 132 GTA CGG CAG CTT TCC TGG GCG CAT GGT CAC GTG CTT TGT GCC TCC GTC AAC TAC CTT CGT 6**4** 152 ACG GTC TCC CTG TAC GTC TCC ACC AAC GCT CTG CTG GCC ATC GCT ATT GAC AGA TAC CTC . 724 172 GCT ATT GTC CAC CCT TTG AAA CCA CGG ATG AAT TAT CAG ACC GCT TCC TTC CTG ATC GCT 784

FIG. 2A

TTG GTC TGG ATG GTC TCC ATC CTC ATC GCT GTC CCA TCT GCC TAC TTC ACC ACA GAA ACC

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ATC CTC GTT ATC GTC AAG AAT CAA GAA AAA ATC TTC TGT GGT CAG ATC TGG TCG GTG GAC 904 232 CAG CAG CTC TAC TAC AAA TCC TAC TTC CTC TTC GTC TTC GGG CTT GAG TTC GTG GGT CCC 914 252 1034 GTG GTC ACT ATG ACC CTG TGC TAT GCC AGG ATC TCC CAA GAG CTC TGG TTC AAG GCT GTA 272 . P R ĸ R CCT GGC TTC CAG ACG GAG CAA ATC CGC AAG CGG CTG CGT TGC CGC CGC AAG ACA GTG CTA 1094 L Y C Y 292 CTG CTC ATG GGC ATC CTC ACA GCC TAC GTG CTG TGC TGG GCG CCG TTC TAT GGC TTT ACC 1144 312 ATA GTG CGA GAC TTC TTC CCC ACG GTA GTT GTG AAG GAG AAG CAC TAC CTC ACC GCC TTC 1204 M 332 TAC GTC GTG GAG TGC ATT GCC ATG AGC AAC AGC ATG ATC AAT ACT ATA TGC TTC GTG ACG 1264 352 GTC AAG AAC AAC ACC ATG AAA TAC TTC AAG AAG ATG CTG CGG CTC CAC TGG CGG CCC TCT 1324 L 372 CAC TAC GGG AGT AAG TCC AGC GCT GAC CTC GAC CTC AAA ACC AGC GGG GTG CCT GCC ACT 1384 E 381 GAA GAG GTG GAT TGT ATC AGA CTA AAG TAG 1414 CCTTCAGGTGTTGCCCAAGGAAAAATTTAACATTCGGTACTCAGTAAATCACACACCATCAACCACTCACAAGCTACAT 1493 GGAAAGATACGGCTGTATTCACGTTCTCCTGCTCTAATGTATCAGGACGCTTCTATGTAATAACATACAGCACAACTGA 1572 1651 CAACCAATTATTCAAGGACAAGAGCTGACATGTGAGAATTACCTGCTATGTGCAAAAAACAAGTTACCCCCCAAAAAAT 1730 1809 GAAAGAAGTCACAAATGACTAGCCAGAGTCATGCTACATATTCTTTCATTCTGTATCTTTTCTGCACAGAACTGTCAAA

GGCAATAGAATAAAGCACCTAGACATACTAGAAATGTAAGGATAACTCCATCAATAGGGAGACCAAGGCCTCATAGGAA	1%7
GAGGGTCCATATAGTATACTGACTTTCCCCACTCCACACCAGTTATCTCCTTAGATATTCTGTACTTATCTGCAATGTT	20 46
GTAATTTCAAATGAGGAAAAATAAGGGGACAGGCTTTACCACAGATGTATCAAATCTCATCAAGCCCATAGGGCAAAGA	2115
TGGGAGGCTCCTGACACAAGAAATGTATCCAGTTCTGGATAACTTTAATGCCAAGCATTTCAGGGCTCTGGGGTCTTGG	2204
AGGAAGAGGACACAGAAAGAGCCGAGGTTTCCAGTGGCAATGAGTATAATCTGTCCATTTGCTATGATTTGGACAATTT	2283
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ATCTCTGTGTGTCTCCACTGTAATGAAATGGAAATAATGAAAAACGGATCATTAGGAACATCAGCCCGGCGAAGTCATGG	2441
TGTGGATGTGATTTTCACCTCTTCCTTTGTGAAGAATGAGGTCGTGAAAAGCTCATTAGAGGGAGTTTGGAATGGAGAA	25 30
ACAGCTCCACACTTTCATCCCTCTTCTTTGAATCGGAGACCACTAAACGCATCTTTGAAGTAGCGTATCTATAGTGAG	2599
GCATAAAGGTCTCCCTGTCACAGAGTGCAATCAAGAAAATACAGTCAATGCCCATACCCTCAGCATCCCTGTGGTCTTA	2678
GACAGTCTTCCCAACAAAGCACTGGTGGACCCCAGGACTGAATTCACTTGTATTATTATGTCATCTACTGAATACTAGG	2757
GTTGATCAAGTTGGCTAGATAGGTATTTTCTTCCTCCTTCACAACCCCATATGTATCCCTCCC	2836
AGGAAGACCTTCTTAAACACAGGAGAACCATTATTCTGTCCAGGACACAAATAACCTCTCCAGTAGACACTGTACCCTT	29 !5
} CACATGTCAACAGAATTTGCCTCCTTGTATTTAAACATATCATCCTCCTTTCATTTAGATTTAACCAGAAACCATT	2994
CCTGTAAATTTCAATGTGTTTGTGATACCGCACTGTAAAAAGCGTATGCTGTTATCATATGGAATAATTAACATACAGA	30 73
ATTGTAATCGTAGTTCCCAAAAGGTTCCCTACTCCTGTTGTATCTTATGTTTATATGTTTGATGTAAATGGAGCTGTGT	3152
AGCTGTCTAAGCAGCTCAAGCCTGAAATGAGGGAATGTCCAATGGTGTTCTTAGAGCAGGCCATCTCAGGCTAGCAGC	32 3 [
PGGCCTCAGTCTGTGCTCTCGGGAGTGTGTTCTTAAATATGAATTAGCAGCAAACCATTAAAAAAAA	3310
ceccec	3347